

27 AVSPKTYKDADFYVAPTQQDVNY__DLVDDFGANGNDTSD 64
 | | | | | | | | | | | | | | | |
 28 DTSEISEVPTELRAAASSFYTPPGQNVRRANKKNLVTDYGVNHNDQND 74
 ↓ ↓
 65 DSNALQRAINAI SRKPNGGILLIPNGTYHFLGIQMKSNVHIRVESDVIK 114
 | | | | | | | | | | | | | | | |
 75 DSSKLNLAIKDLS__DTGGILTLPGKGYLTKIRMRSNVHLEIEKGTIVTY 122
 ↓
 115 PTWN GDGKNHRLFEVG__VNNIVRNFSFQGLGNGFLVDFKDSRDKNLAV 161
 | | | | | | | | | | | | | | | |
 123 PTKGLTPAKNHRIFDFASKTEEKIENASTIVGKGGKFTVDLRGNSSKNQIV 172
 ↓ ↓
 162 FKLGDVRNYKISNFTIDDNKTIFASILVDVTERNGRLHWSRNGIIERIKQ 211
 | | | | | | | | | | | | | | | |
 173 ADVGNVINFKISNFTIKDEKTI FASILVSFTDKAGN_AWPHKGIIENIDQ 221
 ↓ ↓ ↓
 212 NNALFGYGLIQTYGADNILFRNLHSEGGIALRMETDNLMLKNYKQGGIRN 261
 | | | | | | | | | | | | | | | |
 222 ANAHTGYGLIQAYAADNILFNNLSCTGGVTLRLETNLA MKTAKKGGVRD 271
 ↓
 262 IFADNIRCSKGLAAMFGPHFMKNGDVQVINVSSVSCGSAVRSDSGFVEL 311
 | | | | | | | | | | | | | | | |
 272 IFATKIKNINGLTPVMFSPHFMENGKVTIDDVTAIGCAYAVRVEHGFIEI 321
 ↓
 312 FSPTDEVHTRQSWKQAVESKLGRGCAQTPYARGNGGTRWAARVT__OKD 358
 | | | | | | | | | | | | | | | |
 322 FDKGNRASA_DAFKNYIEGILGAGSVEVVYKRNGRT_WAARIANDFNEA 369

 359 ACLDKAKLEYGIEPGSFGTVKVFDVTARF_GYNADLKQDQLDYFSTSNPM 407
 | | | | | | | | | | | | | | | |
 370 AYNHSNPAVSGIKPGKFATSKVINVKATYKGTGAKLKQAFLSYLPCSER_ 418
 ↓
 408 CKRVCLPTKEQWSKQGQTYIGPSLAAVID_TTPETSKYDYDVKTFFNVKRI 457
 | | | | | | | | | | | | | | | |
 419 SK_VCRPGPDGFE____YNGPSLGVTIDNTKRDNSLGNYNMNVSTSSVQ 462

 457 NFPVNSHKTIDINTESSRVONY_YMSECSSSRWER 491
 | | | | | | | | | | | | | | | |
 463 GFPNNYVLNVKYNT__PKVCNQNLG_SITSCN 491

FIG.1

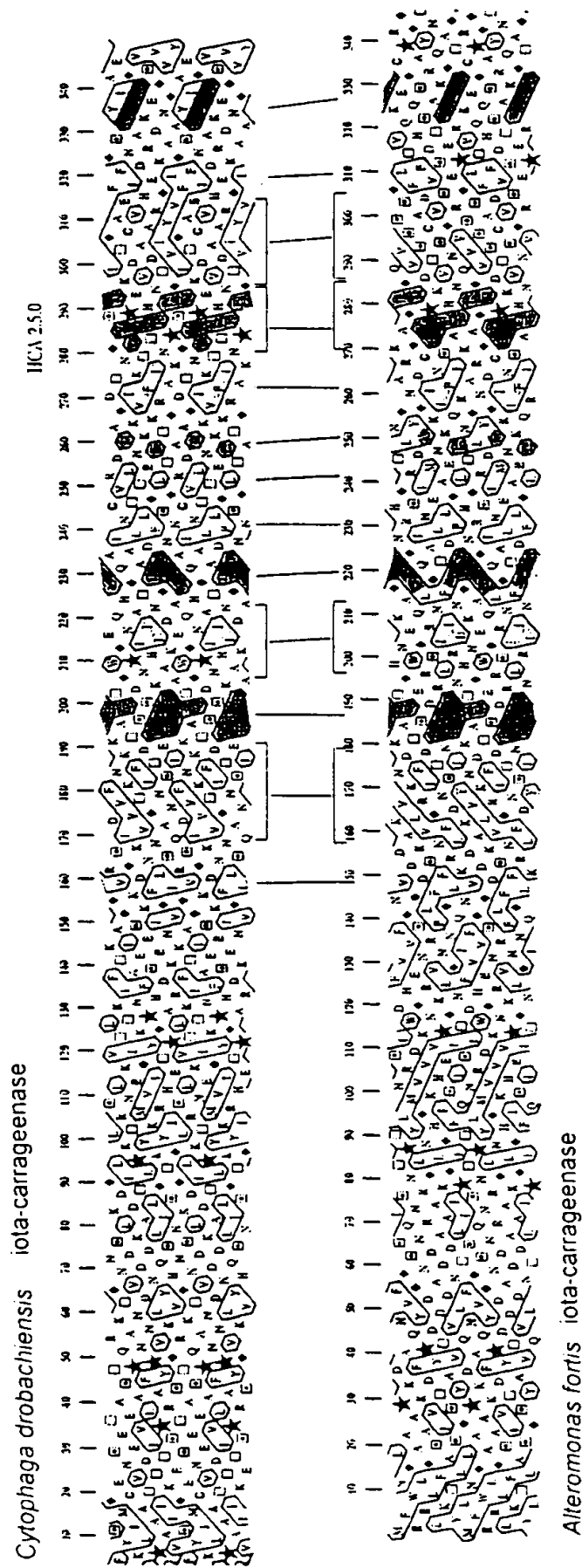
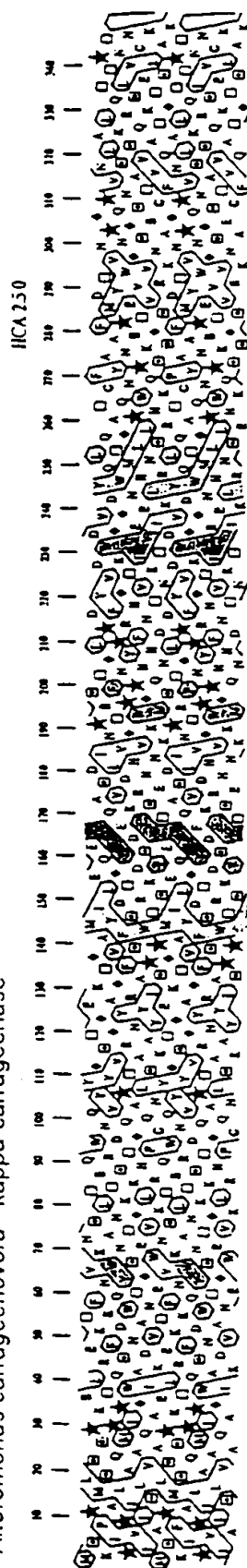


FIG. 2

1	MKKPNFYGKMGR	TALSS	LFYLF	FLGLVY	QQPTK	TSNPND	QWTIK	WSAS	DEFN	KNDPDW	59		
1	MKPISIVAF	PIPAIS	MLLSA	VSQAAS	M_OPPIAK	PGETW	ILQAK	RSDEF	NVK_DAT		55		
60	AKWIK	TGNLP	NTSAW	KWN_NQ	KNVKIS	NGIAEL	TM_RH	NANNT	PPDGGT	YF	108		
56	_KWN	FQTEN	YGVWS	_WK_NEN	AT_V_S	NGKLK	LTTK	RESHQ	RTFWD	GCNQ	QQVANYPLY	109	
109	_TSGIF	KSYQK	FTYGY	FEAKI	QGADIG	EGVCP	SFWLY	SDFDYS	SVAN_GET	VYSEID	VVEL	166	
110	YTS	GVAKS	RATGN	YGYEAR	IKGAST	FPGVSP	AFWMY	STIDR	SLTKE	GDVQY	SEIDVVEL	169	
167	QQFDWY	_EGHOD	DIYDM	DLNLH	AVVKEN	GQGVW	KRPKM	YPQEQ	LNKWR	AM_DP	SKDFHIY	224	
170	TQKSA	VRES	_DH_DL	H_NI_V	VK_NG	KPTW	MRPG	SFPQT	NHNGY	HLPD	PRNDFHTY	221	
225	GCEVN	QNEII	IWYVD	GVE_V	ARKPN	KYWH	RPMM	VTLSL	GLRKP	FVKFF	DNKNNA	INPETDA	283
222	GVNVT	KDKIT	WYVDG	_EIVGE	KONLY	WHRQM	NLTLS	QGLRA	PHTOW	_KCNQ	FYP	SAN	276
284	K_ARE	KLSDI	PTSMY	VDYVR	WEKS	SAGNT	TNPPT	SEVGT	LKTKG	SKLVI	DHWD	ASTGTIS	342
277	KSA_EGF	_PTS	MEVDY	VRTW	VKVG	NNNS	APGEG	QSCPN	TFVAV	NSVQL	SAAKQ	TLRKG	332
343	AVSNNT	KTGQY	AGSVN	NASIA	QIVTL	KANTS	SYKVS	AFGKA	SSPGT	SAYLG	ISKAS	NNELI	402
333	QSTTLE	STVLP	NCATN	KKVIY	SSSNK	QWATV	NSAGV	_KAKN	KGTAT	ITVK	TKNK	GKIDKL	392
403	SNFEF	KTTSY	SKGEI	EIRTN	GVQES	YRIWY	SSGQAY	CDDFN	LVEIN	SGASQ	LNE	NETET	462
393	TI	AVN											397
463	ALEKGI	HIYP	NPYK	NGPLT	IDFGK	PFSGE	VQITG	LNGRT	FLRRN	VVDQT	SVQLLE	SKSKF	522
523	KSGLYI	VKISG	PDGEV	SKILVE									545

FIG.3

Alleromonas carrageenovora kappa-carrageenase



Cytophaga drobachiensis kappa-carrageenase

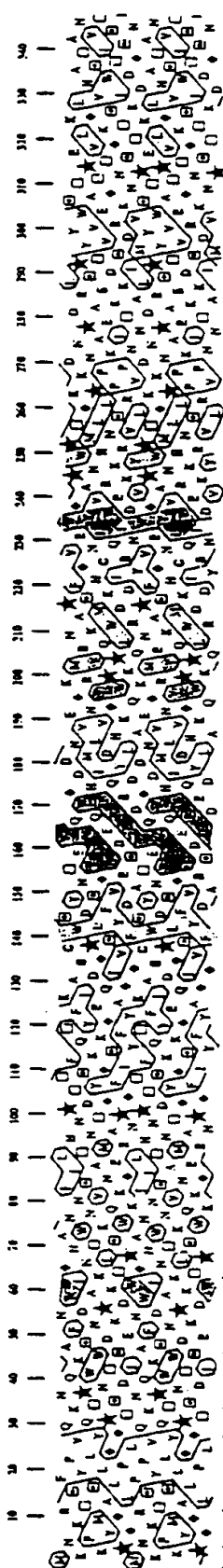


FIG. 4